

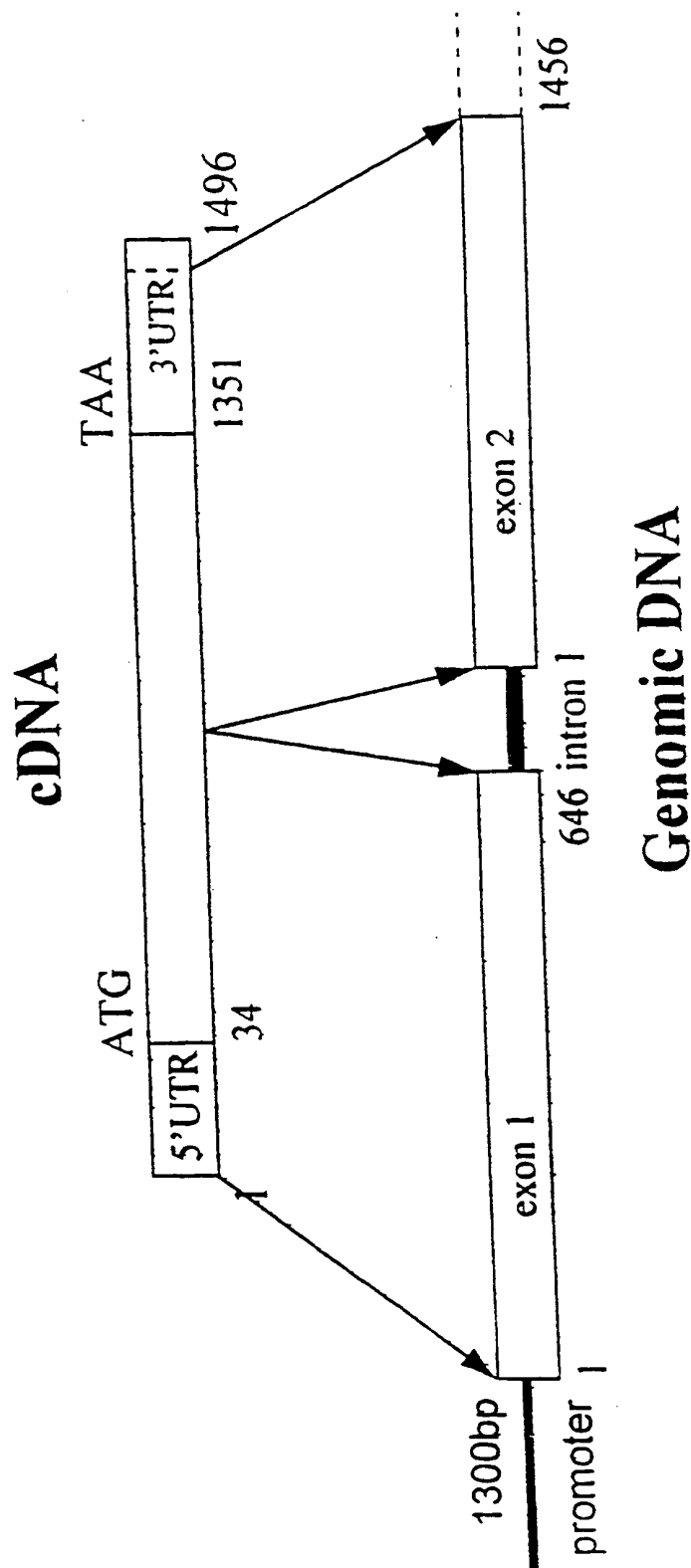
FOOTNOTES

APPROVED	CLASS		SUBCLASS
BY	WO 98/51335		
SUBCLASS			

PCT/CA98/00475

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FIGURE 1



2/24FIGURE 2

	10	20	30	40	50	
MOUSE-X1.DNA	1 ATGAGGCTTC	CTGGTTGGTT	GTGGCTGAGT	TCTGCCGTCC	TCGCTGCCTG	50
HUMAN-X1.DNA	1 ATGAAGCTGG	CTAACTGGTA	CTGGCTGAGC	TCAGCTGTTC	TTGCCACTTA	50
	60	70	80	90	100	
MOUSE-X1.DNA	51 CCGAGC---G	GTGGAGGAGC	ACAACCTGAC	TGAGGGGCTG	GAGGATGCCA	100
HUMAN-X1.DNA	51 CGGTTTTTTG	GTTGTGGCAA	ACAATGAAAC	AGAGGAAATT	AAAGATGAAA	100
	110	120	130	140	150	
MOUSE-X1.DNA	101 GCGCCAGGC	TGCCTGCCCC	GCGAGGCTGG	AGGGCAGCGG	GAGGTGCGAG	150
HUMAN-X1.DNA	101 GAGCAAAGGA	TGTCTGCCCA	GTGAGACTAG	AAAGCAGAGG	GAAATGCGAA	150
	160	170	180	190	200	
MOUSE-X1.DNA	151 GGGA---GCC	AGTGCCCTT	CCAGCTCACC	CTGCCCACGC	TGACCATCCA	200
HUMAN-X1.DNA	151 GAGGCAGGGG	AGTGCCCTTA	CCAGGTAAGC	CTGCCCCCT	TGACTATTCA	200
	210	220	230	240	250	
MOUSE-X1.DNA	201 GCTCCCGCGG	CAGCTTGGCA	GCATGGAGGA	GGTGCTCAAA	GAAGTGCGGA	250
HUMAN-X1.DNA	201 GCTCCCGAAG	CAATTCAGCA	GGATCGAGGA	GGTGTTCAAA	GAAGTCCAAA	250
	260	270	280	290	300	
MOUSE-X1.DNA	251 CCCTCAAGGA	AGCAGTGGAC	AGTCTGAAGA	AATCCTGCCA	GGACTGTAAG	300
HUMAN-X1.DNA	251 ACCTCAAGGA	AATCGTAAAT	AGTCTAAAGA	AATCTTGCCA	AGACTGCAAG	300
	310	320	330	340	350	
MOUSE-X1.DNA	301 TTGCAGGCTG	ACGACCATCG	AGATCCCGGC	GGGAATGGAG	GG-----	350
HUMAN-X1.DNA	301 CTGCAGGCTG	ATGACAACGG	AGACCCAGGC	AGAAACGGAC	TGTTGTTACC	350
	360	370	380	390	400	
MOUSE-X1.DNA	351 -AAT---GGA	GC---AGAGA	CAGCCGAGGA	CAGTAGAGTC	CAGGAACTGG	400
HUMAN-X1.DNA	351 CAGTACAGGA	GCCCCGGGAG	AGGTTGGTGA	TAACAGAGTT	AGAGAATTAG	400
	410	420	430	440	450	
MOUSE-X1.DNA	401 AGAGTCAGGT	GAACAAGCTG	TCCTCAGAGC	TGAAGAATGC	AAAGGACCAG	450
HUMAN-X1.DNA	401 AGAGTGAGGT	TAACAAGCTG	TCCTCTGAGC	TAAAGAATGC	CAAAGAGGAG	450
	460	470	480	490	500	
MOUSE-X1.DNA	451 ATCCAGGGGC	TGCAGGGGCG	CCTGGAGACG	CTCCATCTGG	TAAATATGAA	500
HUMAN-X1.DNA	451 ATCAATGTAC	TTCATGGTCG	CCTGGAGAAG	CTGAATCTTG	TAAATATGAA	500
	510	520	530	540	550	
MOUSE-X1.DNA	501 CAACATTGAG	AACTACGTGG	ACAACAAAGT	GGCAAATCTA	ACCGTTGTGG	550
HUMAN-X1.DNA	501 CAACATAGAA	AATTATGTTG	ACAGCAAAGT	GGCAAATCTA	ACATTGTTG	550
	560	570	580	590	600	
MOUSE-X1.DNA	551 TCAACAGTTT	GGATGGCAAG	TGTTCCAAGT	GTCCCAGCCA	AGAACACATG	600
HUMAN-X1.DNA	551 TCAATAGTTT	GGATGGCAAA	TGTTCAAAGT	GTCCCAGCCA	AGAACAAATA	600
	610	620	630	640	650	
MOUSE-X1.DNA	601 CAGTACAGC	CGG.....	.....	.....	.....	650
HUMAN-X1.DNA	601 CAGTCACGC	CAG.....	.....	.....	.....	650

3/24FIGURE 3

	10	20	30	40	50	
MOUSE-X2.DNA	1 TTCAACATCT	AATATACAAA	GATTGTTCCG	ACCACTACGT	GCTAGGAAGG	50
HUMAN-X2.DNA	1 TTCAACATCT	AATATATAAA	GATTGCTCTG	ACTACTACGC	AATAGGCAAA	50
	60	70	80	90	100	
MOUSE-X2.DNA	51 AGAAGCAGTG	GGGCCTACAG	AGTTACCCCT	GATCACAGAA	ACAGCAGCTT	100
HUMAN-X2.DNA	51 AGAAGCAGTG	AGACCTACAG	AGTTACACCT	GATCCCAAAA	ATAGTAGCTT	100
	110	120	130	140	150	
MOUSE-X2.DNA	101 TGAGGTCTAC	TGTGACATGG	AGACCATGGG	TGGAGGCTGG	ACGGTGCTGC	150
HUMAN-X2.DNA	101 TGAAGTTTAC	TGTGACATGG	AGACCATGGG	GGGAGGCTGG	ACAGTGCTGC	150
	160	170	180	190	200	
MOUSE-X2.DNA	151 AGGCTCGCCT	TGATGGCAGC	ACCAACTTCA	CCAGAGAGTG	GAAAGACTAC	200
HUMAN-X2.DNA	151 AGGCACGTCT	CGATGGGAGC	ACCAACTTCA	CCAGAACATG	GCAAGACTAC	200
	210	220	230	240	250	
MOUSE-X2.DNA	201 AAAGCCGGCT	TTGGAAACCT	TGAACGAGAA	TTTTGGTTGG	GCAACGATAA	250
HUMAN-X2.DNA	201 AAAGCAGGCT	TTGGAAACCT	CAGAAGGGAA	TTTTGGCTGG	GGAACGATAA	250
	260	270	280	290	300	
MOUSE-X2.DNA	251 AATTCATCTT	CTGACCAAGA	GTAAGGAAAT	GATTTTGAGA	ATAGATCTTG	300
HUMAN-X2.DNA	251 AATTCATCTT	CTGACCAAGA	GTAAGGAAAT	GATTCTGAGA	ATAGATCTTG	300
	310	320	330	340	350	
MOUSE-X2.DNA	301 AAGACTTTAA	TGGTCTCACA	CTTTATGCCT	TGTATGATCA	GTTTTATGTG	350
HUMAN-X2.DNA	301 AAGACTTTAA	TGGTGTGCAA	CTATATGCCT	TGTATGATCA	GTTTTATGTG	350
	360	370	380	390	400	
MOUSE-X2.DNA	351 GCTAATGAAT	TTCTCAAATA	CCGATTACAC	ATCGGTAACT	ACAATGGCAC	400
HUMAN-X2.DNA	351 GCTAATGAGT	TTCTCAAATA	TCGTTTACAC	GTTGGTAACT	ATAATGGCAC	400
	410	420	430	440	450	
MOUSE-X2.DNA	401 GGCAGGGGAT	GCCTTGCGTT	TCAGTCGACA	CTACAACCAT	GACCTGAGGT	450
HUMAN-X2.DNA	401 AGCTGGAGAT	GCATTACGTT	TCAACAAACA	TTACAACCAC	GATCTGAAGT	450
	460	470	480	490	500	
MOUSE-X2.DNA	451 TTTTCACAAC	CCCAGACAGA	GACAACGATC	GGTACCCCTC	TGGGAACTGT	500
HUMAN-X2.DNA	451 TTTTCACCAC	TCCAGATAAA	GACAATGATC	GATATCCTTC	TGGGAACTGT	500
	510	520	530	540	550	
MOUSE-X2.DNA	501 GGGCTCTATT	ACAGCTCAGG	CTGGTGGTTT	GATTCATGTC	TCTCTGCCAA	550
HUMAN-X2.DNA	501 GGGCTGTACT	ACAGTTCAGG	CTGGTGGTTT	GATGCATGTC	TTTCTGCCAA	550
	560	570	580	590	600	
MOUSE-X2.DNA	551 CTTAAATGGC	AAATATTACC	ACCAGAAATA	CAAAGGTGTC	CGTAATGGGA	600
HUMAN-X2.DNA	551 CTTAAATGGC	AAATATTATC	ACCAAAAATA	CAGAGGTGTC	CGTAATGGGA	600
	610	620	630	640	650	
MOUSE-X2.DNA	601 TTTTCTGGGG	CACCTGGCCT	GGTATAAACC	AGGCACAGCC	AGGTGGCTAC	650
HUMAN-X2.DNA	601 TTTTCTGGGG	TACCTGGCCT	GGTGTAAAGT	AGGCACACCC	TGGTGGCTAC	650
	660	670	680	690	700	
MOUSE-X2.DNA	651 AAGTCCTCCT	TCAAACAGGC	CAAGATGATG	ATTAGGCCCA	AGAATTTCAA	700
HUMAN-X2.DNA	651 AAGTCCTCCT	TCAAAGAGGC	TAAGATGATG	ATCAGACCCA	AGCACTTTAA	700
	710	720	730	740	750	
MOUSE-X2.DNA	701 GCCATAA...	.....	.....	.....	.....	750
HUMAN-X2.DNA	701 GCCATAA...	.....	.....	.....	.....	750

FIGURE 5

		10	20	30	40	50	
MOUSEPRO.AMI	1	GRPGALNLS	SAVLAACR-A	VEEHQLTEGL	EDASQAQAF	ARLEGSRRDF	50
HUMANPRO.AMI	1	GRUANRYNLS	SAVLATYGF	IVANETETEI	KDERAKDVCI	VRLESRKCE	50
		60	70	80	90	100	
MOUSEPRO.AMI	51	-GSCCFELT	LFTLTIOLEP	ILGSMEEVLA	EVRTLKEAVD	SLKSKCODCK	100
HUMANPRO.AMI	51	EAGECFYVS	LFP LTIOLPK	EFRIEEVFA	EVQNLKEIIN	SLKSKCODCK	100
		110	120	130	140	150	
MOUSEPRO.AMI	101	LOADDHRDPG	GNG-----GN	GAETAELSRV	QELESVNKI	SSELKNAKDQ	150
HUMANPRO.AMI	101	LOADDNGDPG	RNGLLLPSTG	APGEVGNRV	RELESEVNKL	SSELKNANEE	150
		160	170	180	190	200	
MOUSEPRO.AMI	151	IQGLQSRLET	LHLVNMMNIE	NYVDNKVANI	IVVNSLDGK	CSKCPSOEHM	200
HUMANPRO.AMI	151	INVLIHGRLEK	LNLVNMMNIE	NYVDSKVANI	IVVNSLDGK	CSKCPSOEQI	200
		210	220	230	240	250	
MOUSEPRO.AMI	201	DSQPVOHLIY	KDCSDHYVLS	RRSSGAYRVT	PDHRNSSFV	YCDMETMGGG	250
HUMANPRO.AMI	201	DSRPVOHLIY	KDCSEYTAIS	KRSSETYRVT	PDPRNSSFV	YCDMETMGGG	250
		260	270	280	290	300	
MOUSEPRO.AMI	251	NTVLQARLDG	STNFTREAKE	YKAGFGNLEP	EFWLGNDKIH	LLTKSKEMIL	300
HUMANPRO.AMI	251	NTVLQARLDG	STNFTPTAQL	YKAGFGNLEP	EFWLGNDKIH	LLTKSKEMIL	300
		310	320	330	340	350	
MOUSEPRO.AMI	301	RIDLEDENGL	TLIALYDOFY	VANEFLLKYRL	IVSNYNGTAG	DALRFRNKHYN	350
HUMANPRO.AMI	301	RIDLEDENGV	ELIALYDOFY	VANEFLLKYRL	IVSNYNGTAG	DALRFRNKHYN	350
		360	370	380	390	400	
MOUSEPRO.AMI	351	HDLRFFFTPD	RDNDRYPGSGN	GLIYSSGWW	FDSCLSANLN	SKYYHOKYKE	400
HUMANPRO.AMI	351	HDLKFFFTPD	KDNDRYPGSGN	GLIYSSGWW	FDSCLSANLN	SKYYHOKYKE	400
		410	420	430	440	450	
MOUSEPRO.AMI	401	VRNGIFWGTW	PGINQAQPGG	YKSSFKAKM	MIRPKNEKP*	.....	450
HUMANPRO.AMI	401	VRNGIFWGTW	PGVSEAHPGG	YKSSFKAKM	MIRPKNEKP*	.....	450

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FIGURE 6

	10	20	30	40	50	
MOUSEPRO.AMI	1	MRLPGWLWLS	SAVLAACR-A	VEEHNLTGL	EDASQAACP	ARLESGRCE 50
HUMANPRO.AMI	1	MKLANWYWLS	SAVLATYGL	VVANNETEEI	KDERAKDVCP	VRLESRGKCE 50
	60	70	80	90	100	
MOUSEPRO.AMI	51	-GSQCPFQLT	LPTLTIQLEP	QLGSMEEVLK	EVRTLKEAVD	SLKKSCQDCK 100
HUMANPRO.AMI	51	EAGECPYQVS	LPPLTIQLEK	QFSRIEEVFK	EVQNLKEIVN	SLKKSCQDCK 100
	110	120	130	140	150	
MOUSEPRO.AMI	101	LQADDHRDPG	GNG-----GN	GAETAEDSRV	QELESQVNKL	SSELKNAKDQ 150
HUMANPRO.AMI	101	LQADDNGDPG	RNGLLLPSTG	APGEVGDNRV	RELESEVNKL	SSELKNAKEE 150
	160	170	180	190	200	
MOUSEPRO.AMI	151	IQGLQGRLET	LHLVNMNIE	NYVDNKVANL	TVVNSLDGK	CSKCPSQEHM 200
HUMANPRO.AMI	151	INVLHGRLEK	LNLVNMNIE	NYVDSKVANL	TFVNSLDGK	CSKCPSQEQI 200
	210	220	230	240	250	
MOUSEPRO.AMI	201	QSQPVQHLYI	KDCSDHYVLG	RRSSGAYRVT	PDHRNSSFEV	YCDMETMGGG 250
HUMANPRO.AMI	201	QSRPVQHLYI	KDCSDYYAIG	KRSSETYRVT	PDPKNSSFEV	YCDMETMGGG 250
	260	270	280	290	300	
MOUSEPRO.AMI	251	WTVLQARLDG	STNFTREWKD	YKAGFGNLER	EFWLGNDKIH	LLTKSKEMIL 300
HUMANPRO.AMI	251	WTVLQARLDG	STNFTRTWQD	YKAGFGNLR	EFWLGNDKIH	LLTKSKEMIL 300
	310	320	330	340	350	
MOUSEPRO.AMI	301	RIDLEDFNGL	TLYALYDQFY	VANEFLKYRL	HIGNYNGTAG	DALRFSRHYN 350
HUMANPRO.AMI	301	RIDLEDFNGV	ELYALYDQFY	VANEFLKYRL	HVGNYNGTAG	DALRFNKHYN 350
	360	370	380	390	400	
MOUSEPRO.AMI	351	HDLRFFFTPD	RDNDRYPSGN	CGLYSSSGWW	FDSCLSANLN	GKYYHQYKYG 400
HUMANPRO.AMI	351	HDLKFFFTPD	KDNDRYPSGN	CGLYSSSGWW	FDACLSANLN	GKYYHQYKYG 400
	410	420	430	440	450	
MOUSEPRO.AMI	401	VRNGIFWGTW	PGINQAQPGG	YKSSFQAKM	MIRPKNFKP*	..... 450
HUMANPRO.AMI	401	VRNGIFWGTW	PGVSEAHPPG	YKSSFKEAKM	MIRPKHFKP*	..... 450

### FIGURE 7

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	15.5	5.5	10	25
Health status	1.5	0.5	1	2
Stress level	2.5	1.5	1	4
Life satisfaction	3.5	1.5	1	5
Work satisfaction	3.5	1.5	1	5
Family satisfaction	3.5	1.5	1	5
Community satisfaction	3.5	1.5	1	5
Overall satisfaction	3.5	1.5	1	5

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## FIGURE 8

		10	20	30	40	50	
MOUSEPRO.DNA	1	TCGGTTTGGG	TATCATGGGA	TG-GAATGAG	AAGGGA-AAG	TAGGAGCCCCG	50
HUMANPRO.DNA	1	TAGGGTTGGA	AGCCAGGTCT	CCTGAGTATG	CGAGAATAAA	TACAGTCATG	50
		60	70	80	90	100	
MOUSEPRO.DNA	51	AGAGTGC GGT	AAGACAA--G	GCATAAGGCG	TGTCTGACAA	ATTCTTCATA	100
HUMANPRO.DNA	51	GAAGTGTA	GAGTCTGCCA	ACATTTTGAG	AATGTGAATA	GGATTTGGC-	100
		110	120	130	140	150	
MOUSEPRO.DNA	101	CACACATTT	CCCTTTGCAC	ATTGAGTCTG	TATAGGTTAT	TTCTATAGGA	150
HUMANPRO.DNA	101	TA-AAATTA	GGGATATAC	AGAAAAGTCA	TAGGAAATCA	GGTTAAAGAC	150
		160	170	180	190	200	
MOUSEPRO.DNA	151	GAATAAAT	ATTCAAATTC	CTGTGCACT	G-GTAACAGG	CATGAAGGCT	200
HUMANPRO.DNA	151	ATAAATAT	GATAGGCTAC	AGAGTGT TTT	AAGTAATACA	ATAAACATT	200
		210	220	230	240	250	
MOUSEPRO.DNA	201	CAGCAAAGCC	AATACGTGTT	ATGTCCAGTT	GGAGACAGTG	CCAGGGCCAA	250
HUMANPRO.DNA	201	TAG--ATTT	TGCCATGTC	A-GTCATTTT	GAAATTATTT	TTAAAGCAAA	250
		260	270	280	290	300	
MOUSEPRO.DNA	251	CATTCCAGAC	TTCTCAGATA	GAAAGTGCGC	CTGCCTGCCC	-TGCTCTGAG	300
HUMANPRO.DNA	251	AAAACC---C	TTTTTAAACA	AGAAATCTTA	TGAGATGTCA	ATATGCAAAA	300
		310	320	330	340	350	
MOUSEPRO.DNA	301	--AATTGAA	GAGAGTAGTT	C---AGTTA	GAATTAAGAG	GCAGTAGAGA	350
HUMANPRO.DNA	301	CAAATTAAAA	GGAGGTGGTT	TCTCTAAGTG	AAGCTGTTCC	TCTTCTCTGC	350
		360	370	380	390	400	
MOUSEPRO.DNA	351	AA--AGTCTT	GGGAAATCTG	GTTAGAGA--	TATAAATATG	AGAACTGGAC	400
HUMANPRO.DNA	351	CTTCAGCCTC	TGAAGAGAAA	GTTAGAAAAC	TATTATCATT	AATGCTACAT	400
		410	420	430	440	450	
MOUSEPRO.DNA	401	ATGGTGGTAC	ACACCTGTGA	TCTCTGTGTT	TAGGAGGGAG	AGGCAGAGAG	450
HUMANPRO.DNA	401	GTTTTGA-AC	AAGCTGATAT	ACCAAGTGGC	CCAGAGAGC-	AGGTAGAAGA	450
		460	470	480	490	500	
MOUSEPRO.DNA	451	ATCAGGAGTT	CAAGGCCAGC	CTGAGCTACT	TGAGACCCAG	TCTAAATAAA	500
HUMANPRO.DNA	451	ACCAGCG---	TGGAGACAGA	--AAGCAA--	-GAGGCCG-G	CCTGCCAGGG	500
		510	520	530	540	550	
MOUSEPRO.DNA	501	TAAGAGATAG	ATTACAGAGT	GCCTTTAACT	AGTACAGAGA	AAGAATTTGG	550
HUMANPRO.DNA	501	CTACCTGCAG	AA-AGAAAGG	GCAAAGATGC	TGTAGGCAAG	AGAAGTTCAG	550
		560	570	580	590	600	
MOUSEPRO.DNA	551	GT TATCTGT	GTCAGTTACG	CTGAAATAAT	TTTTAAGTAA	TAAATCCCT	600
HUMANPRO.DNA	551	GACAGACACT	GGCA--TA-G	CTCAAA-GAT	TCACATTTGA	GCAG-----C	600
		610	620	630	640	650	
MOUSEPRO.DNA	601	TTTAATAAGA	AACCTTATGA	G-GTCAGTAT	GCACAATGAA	CTTAAGAGAG	650
HUMANPRO.DNA	601	TGTGGAAGAT	GACAGTACAA	TTACCAAAAT	GT-CGAAGGG	C--AAAGGAG	650
		660	670	680	690	700	
MOUSEPRO.DNA	651	ACCCCCAGCT	CCTGAGCTGA	GTGATGGGGA	AGGACAGCCA	CTGCCTGTGA	700
HUMANPRO.DNA	651	GC----AGCT	ACTGGTTT--	-TGATG---A	AAGACAATTA	TGTCCTTT--	700
		710	720	730	740	750	
MOUSEPRO.DNA	701	TGTGTGAGTG	ACGTGCTTCC	AAGTGT TTTA	ACCACTGACG	ATTACATAGC	750
HUMANPRO.DNA	701	TAAATGGGTC	TTAGACATTT	AGACATTTAT	AT-AC--ACT	ATGCTACGGA	750
		760	770	780	790	800	
MOUSEPRO.DNA	751	CTGCACAGTC	AGGAGAAAAC	AGCCGTATTC	TCTGCCAGTT	CTCTTCCCTT	800
HUMANPRO.DNA	751	CAAAGGAAT-	AGAAAGTAGC	A-CTTTTTC	TCCACTAGTT	TTCTTCTCTT	800
		810	820	830	840	850	
MOUSEPRO.DNA	801	TTACAAACAG	ATGAGAGACA	CACACAGAGA	ATCCATT TAA	AGAGCGGACC	850
HUMANPRO.DNA	801	TTTCAAGTAG	ATGAAGCAAA	AGT-CAACTG	CAATAGTCAG	AAAGCTGTAC	850
		860	870	880	890	900	

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FIGURE 8 cont'd

MOUSEPRO.DNA	851	TTTGTTCTGA	TTAGGGGCAA	TTTAAAGTAC	TTAAGAGTTC	ACACAAAGTC	900
HUMANPRO.DNA	851	TTTGTTACAC	TTAGAAACTT	CTAAAAGTGC	TTAAGATTTC	ACCTGAAAGT	900
		910	920	930	940	950	
MOUSEPRO.DNA	901	TAGCCTTCAA	AAAGAAAACA	GGTCCCAAA	----CTA---	-GGGAGGAAA	950
HUMANPRO.DNA	901	CCAACAT-GA	AGAAAATACA	GGCTCCCAAA	TGCCCCATTC	TAAGAAGAAA	950
		960	970	980	990	1000	
MOUSEPRO.DNA	951	CAGAATCATT	TCCATTTTGG	TGACATTTA-	GTGGGAAGAA	GCTCACAGAC	1000
HUMANPRO.DNA	951	AAGGACCATT	TTCATTTTGG	TAACGTTTCT	GTTCTATAGA	CAGTTTGGAT	1000
		1010	1020	1030	1040	1050	
MOUSEPRO.DNA	1001	ATTTAGACGT	TCCAACCTCT	TCCCCACTAG	TG-----G	ACCAAGT-AT	1050
HUMANPRO.DNA	1001	AACTAGCTCT	TACTTTTTAT	CTTTAAAAAC	TGTTTTTCCA	GTGAAGTTAC	1050
		1060	1070	1080	1090	1100	
MOUSEPRO.DNA	1051	ATAATATGGT	ATCTTTTGGG	CACTGGTATT	ACAA-CTGTT	TTTTAAACAA	1100
HUMANPRO.DNA	1051	GTATAATTAT	TTACTTCAAG	CG-TAGTATA	CCAAATTACT	TTAGAAATGC	1100
		1110	1120	1130	1140	1150	
MOUSEPRO.DNA	1101	AAGACTTTTC	TTGTGCTTTA	CTAAAAAC-C	CA-GACGGTG	AATCTTGAAT	1150
HUMANPRO.DNA	1101	AAGACTTTTC	TTATACTTCA	TAAAATACAT	TATGAAAGTG	AATCTTG--T	1150
		1160	1170	1180	1190	1200	
MOUSEPRO.DNA	1151	ACAATGCGTG	GCACCCACGG	CAGGCATTCT	ATTGTGCATA	GTTTTGACTG	1200
HUMANPRO.DNA	1151	TGGCTGTGTA	CATTTGACTA	TAATAATTTT	AATGCATATT	ATTTCTATTG	1200
		1210	1220	1230	1240	1250	
MOUSEPRO.DNA	1201	ACAGGAGATG	ACAGCATTTG	GCTGGCTGCG	CTTGCTGAGG	ACCCCTCTCT	1250
HUMANPRO.DNA	1201	AGAGTAAGTT	ACAGTTTTTG	GCAAACCTGCG	TTTGATGAGG	GCTATCTCTT	1250
		1260	1270	1280	1290	1300	
MOUSEPRO.DNA	1251	CCTG-TGTG-	GCGTCTGAGA	CT-GTGATGC	AAATGCGCCC	GCCCTTTTCT	1300
HUMANPRO.DNA	1251	CTTCCTGTGC	GTTTCTAAAA	CTTGATGATGC	AAACGCTCCC	ACCCCTTCTT	1300
		1310	1320	1330	1340	1350	
MOUSEPRO.DNA	1301	GGGAACCTCAG	AACGCCTGAG	TCAGGCGGCG	GTGGCTATTA	AAGCG-----	1350
HUMANPRO.DNA	1301	GGGAACACAG	AAAGCCTGAC	TCAGGCCATG	GCCGCTATTA	AAGCAGCTCC	1350
		1360	1370	1380	1390	1400	
MOUSEPRO.DNA	1351	---CCTGGTC	AG-----GCT	GGGCT-GCCG	CACTGCAAGG	ATG.....	1400
HUMANPRO.DNA	1351	AGCCCTGCGC	ACTCCCTGCT	GGGTGAGCAG	CACTGTAAAG	ATG.....	1400



### FIGURE 9

**SUBSTITUTE SHEET (RULE 26)**

[illegible]

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FIGURE 9 CONT'D

810            820            830            840            850  
 TTTGTTACACTTAGAACTTCTAAAAGTGCTTAAGATTT~~CACCTGAAACG~~  
                                          TCF1                                           BHLH  
 860            870            880            890            900  
 CCAACATGAAGAAAATACAGGCTCCCCAATGCCCCATTCTAAGAAGAAAA  
 910            920            930            940            950  
 AGGACCATTTTCATTTTAGTAACGTTTCTGTTCTATAGACAGTTTGGATA  
 960            970            980            990            1000  
 ACTAGCTCTTACTTTTTATCTTTAAAACTGTTTTTCCAGTGAAGTTACG  
 1010           1020           1030           1040           1050  
 TATAATTATTTACTTCAAGCGTAGTATACCAAATTACTTTAGAAATGCAA  
                                                                                  NF IL6  
 1060           1070           1080           1090           1100  
 GACTTTTCTTATACTTCATAAAATACATTATGAAAGTGAATCTTGTTGGC  
                                                                                  NF IL6  
 1110           1120           1130           1140           1150  
 TGTGTACATTTGACTATAATAATTTCAATGCATATTATTTCTATTGAGAG  
                                                                                  BHLH  
 1160           1170           1180           1190           1200  
 TAAGTTACAGTTTTTGGCAAACCTGCGTTTGATGAGGGCTATCTCCTCTTC  
 1210           1220           1230           1240           1250  
 CTGTGCGTTTCTAAAACCTGATGCAAACGCTCCCACCCTTTCCTGGGA  
                                                                                  AABS  
 1260           1270           1280           1290           1300  
 ACACAGAAACGCTGACTCAGGCACGTGCCGCTATTAAAGCAGCTCCAGCC  
 +1            AP 1            BHLH            TATA box  
 1310           1320           1330  
 CTGCGCACTCCCTGCTGGGTGAGCAGCACTGTAAAGATG

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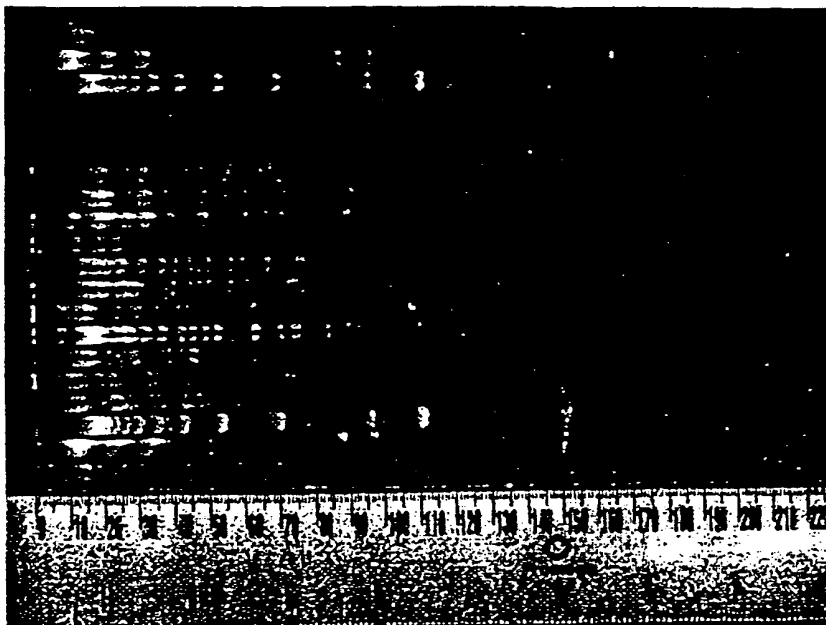


FIGURE 10B

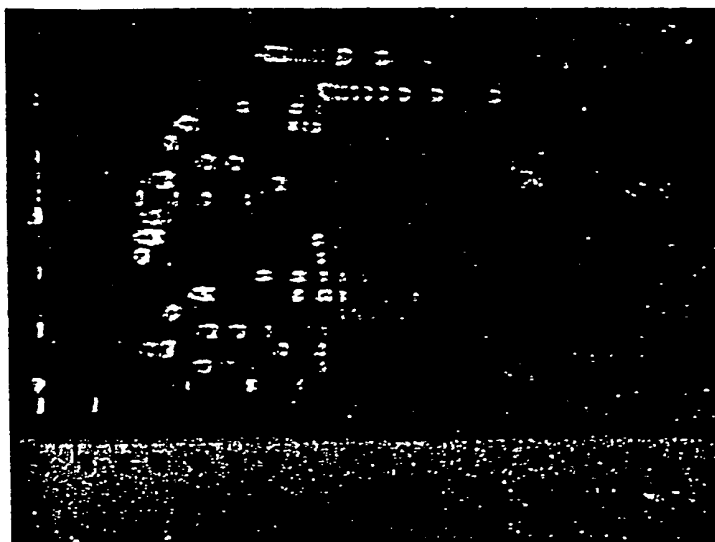
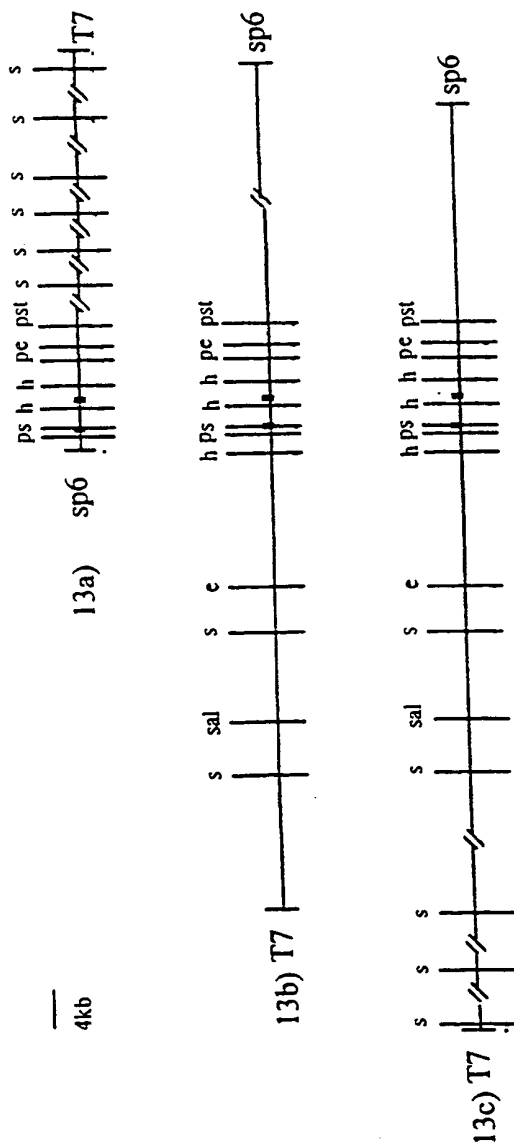


FIGURE 10A

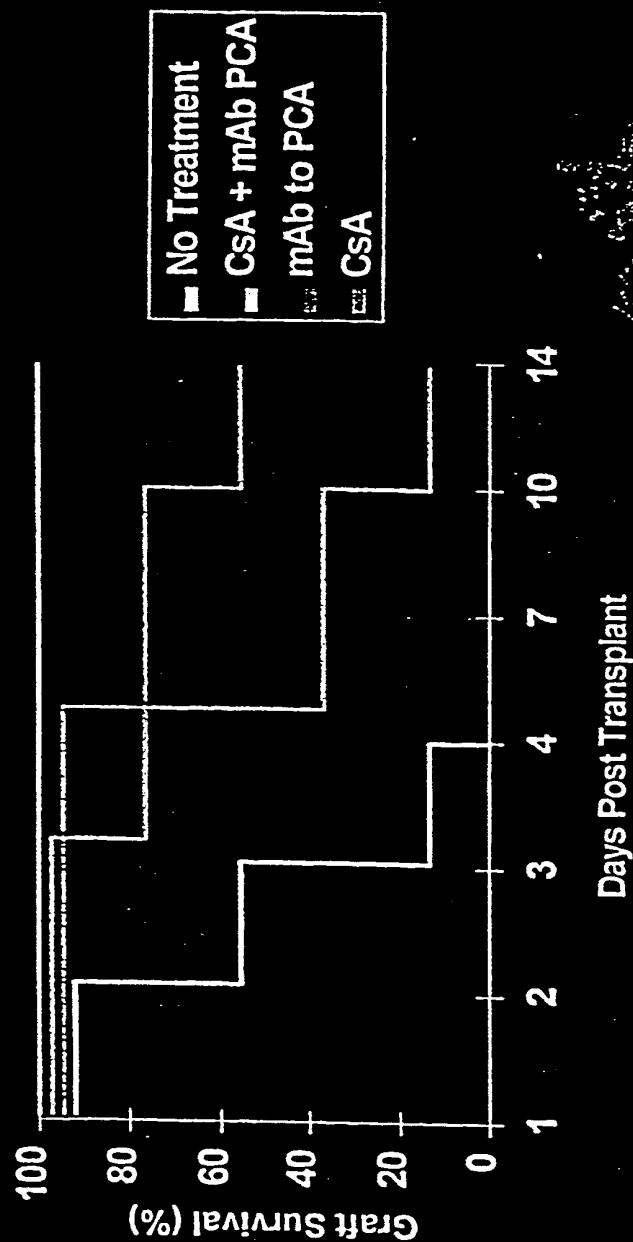
**FIGURE 11**



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**FIGURE 12**

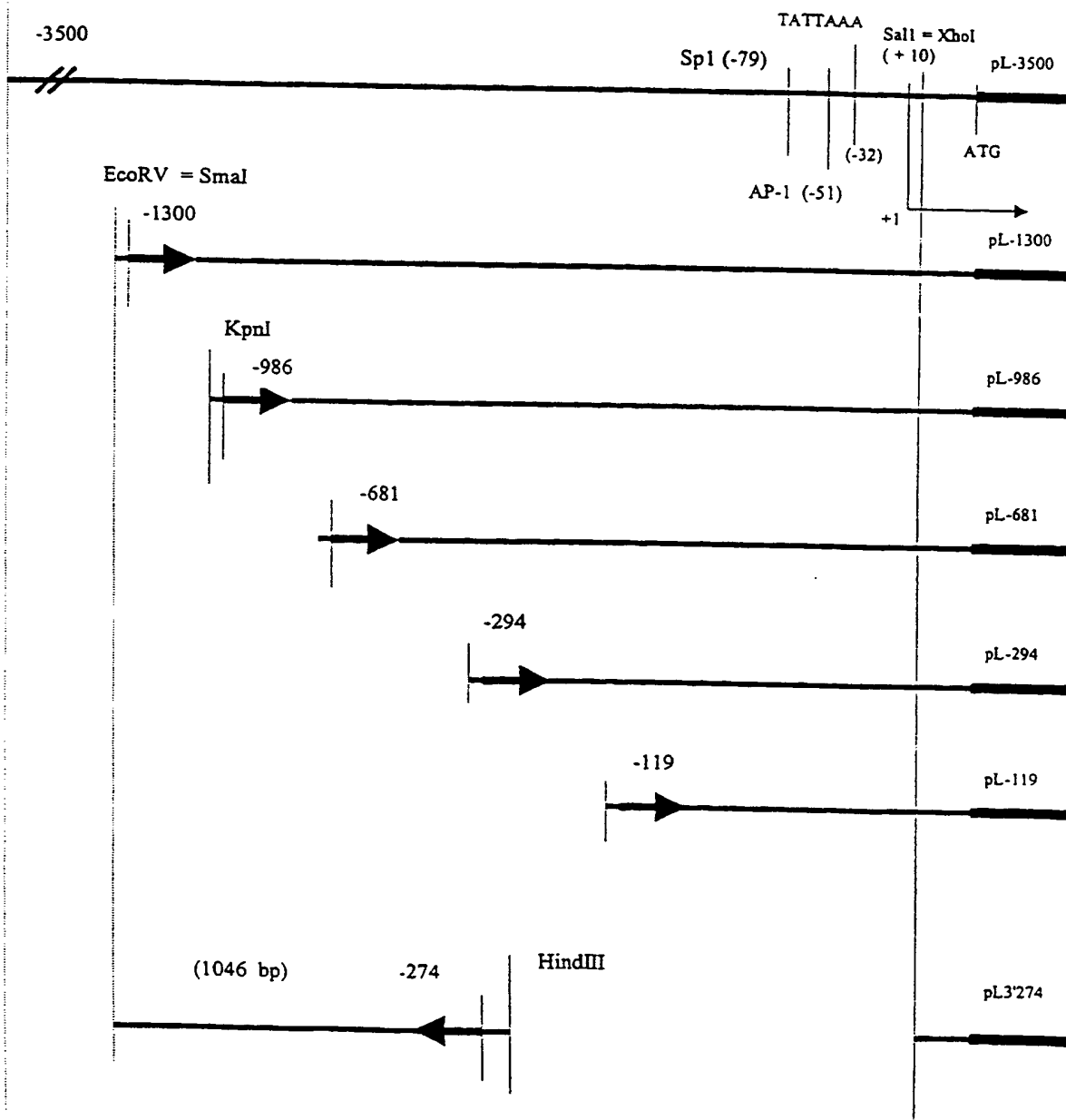
**Prevention of CsA Graft Rejection by CsA Alone or in Combination with Antibodies to Immune Coagulants**



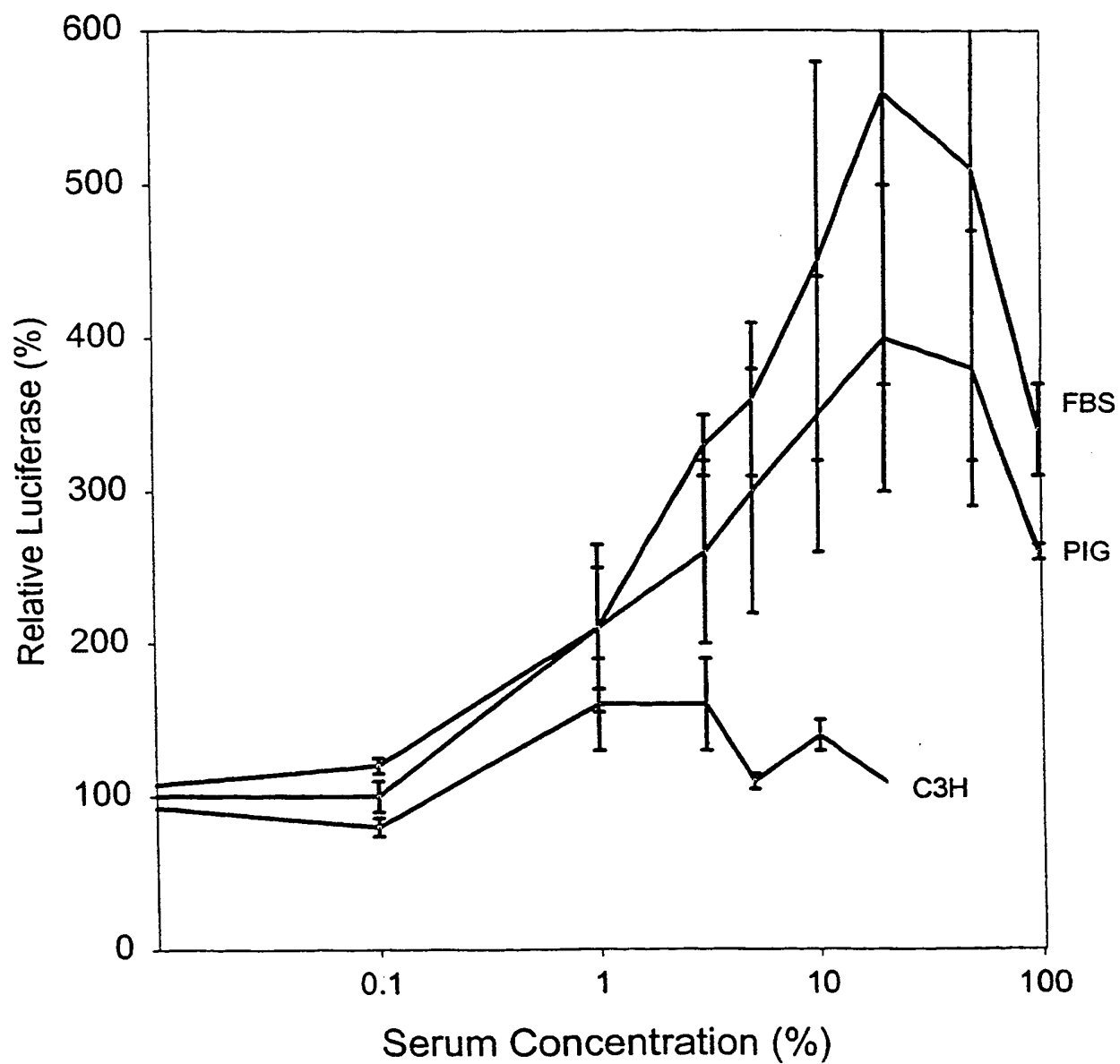
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**FIGURE 13**

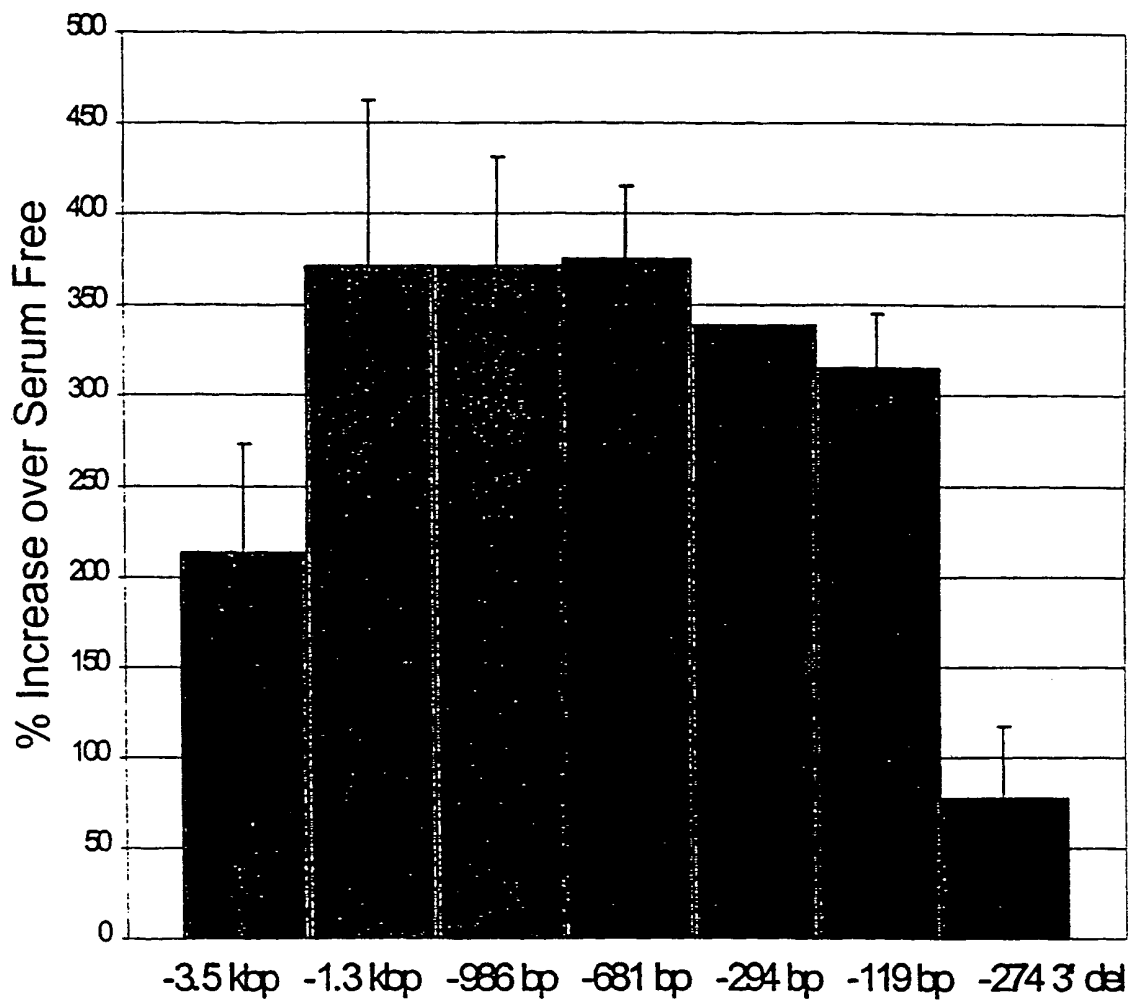
NotI (blunted)= SmaI



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**FIGURE 15**

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FIGURE 16

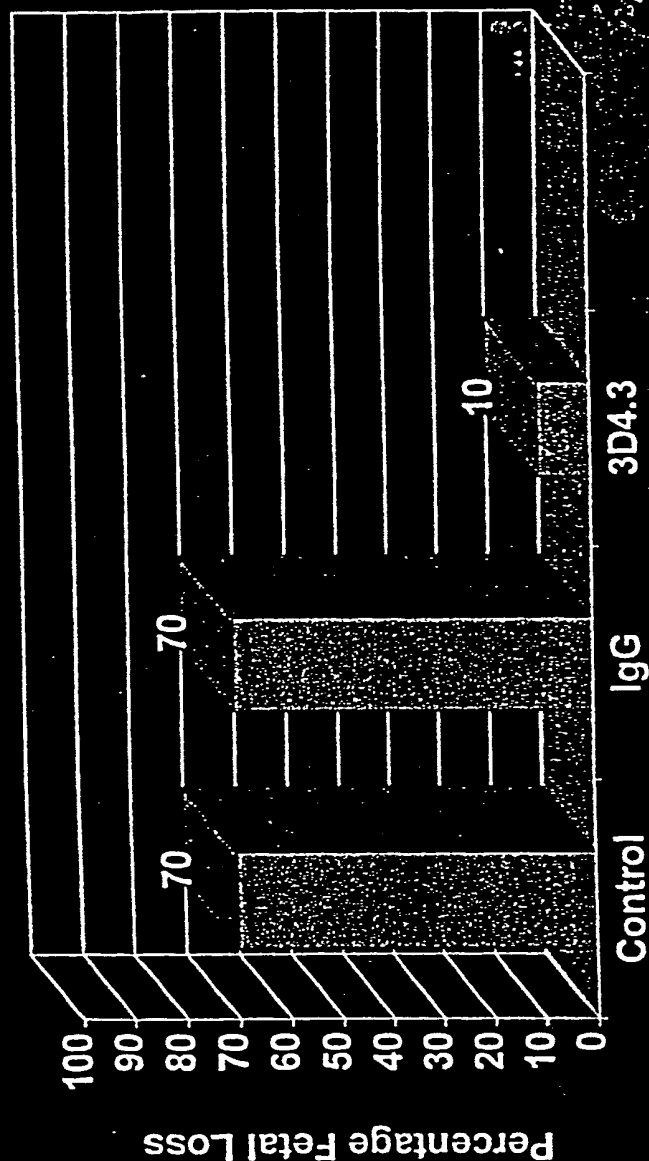


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FOETAL LOSS

FIGURE 18

# Prevention of Fetal Loss by Monoclonal Antibody 3D4.3



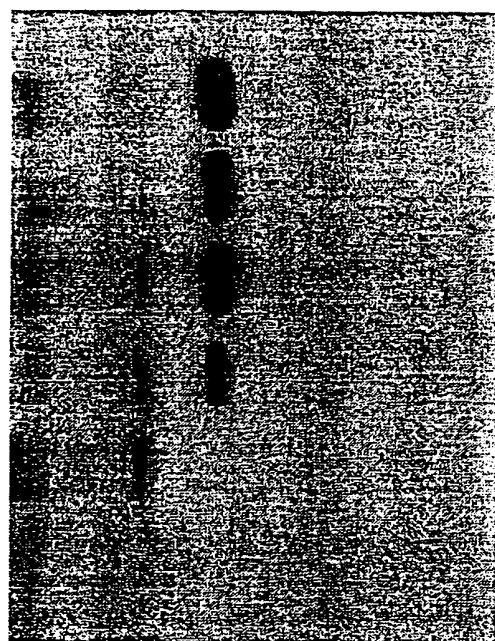
Antibody (10  $\mu$ g/day I.V. given for 14 days)



Xenotransplantation Canada

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FIGURE 19



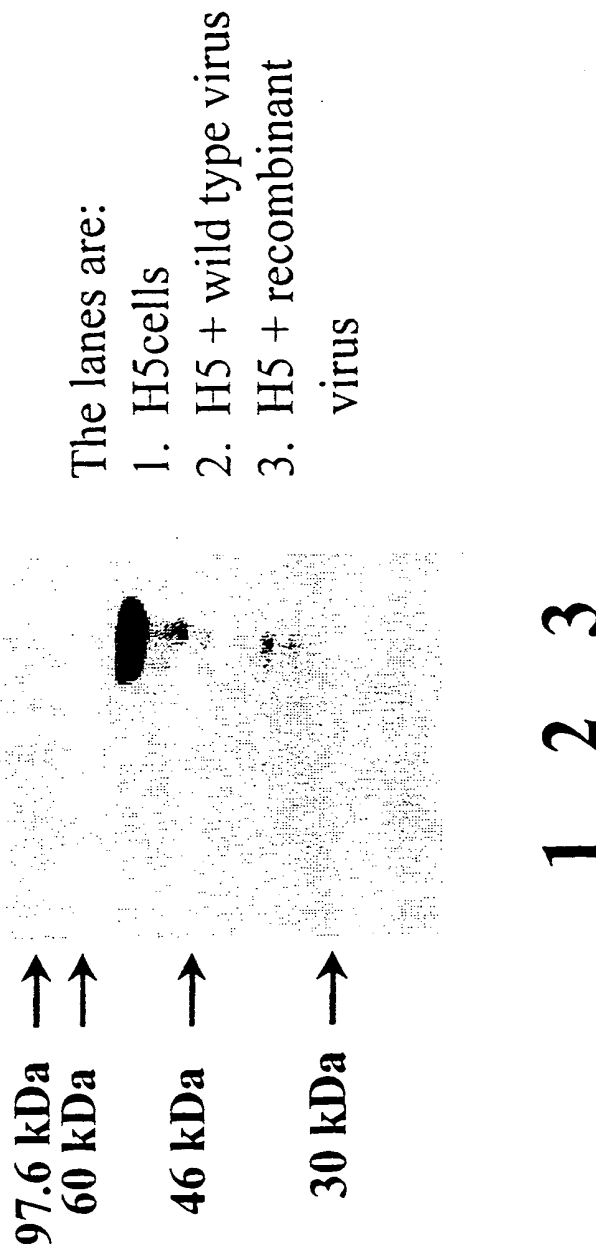
h postinfection

0 12 24 48 72 96 120

97.6 kDa ↑  
60 kDa ↑  
46 kDa ↑  
30 kDa ↑

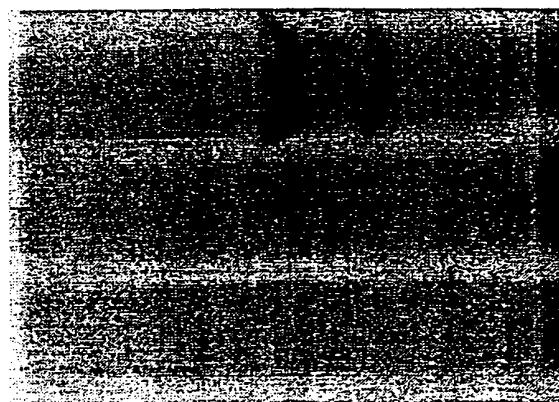
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FIGURE 20



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FIGURE 21



The lanes are:  
 1. H5cells  
 2. H5 + wild type virus  
 3. H5 + recombinant virus

97.6 kDa →  
 60 kDa →  
 46 kDa →  
 30 kDa →

1 2 3

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**FIGURE 22**

